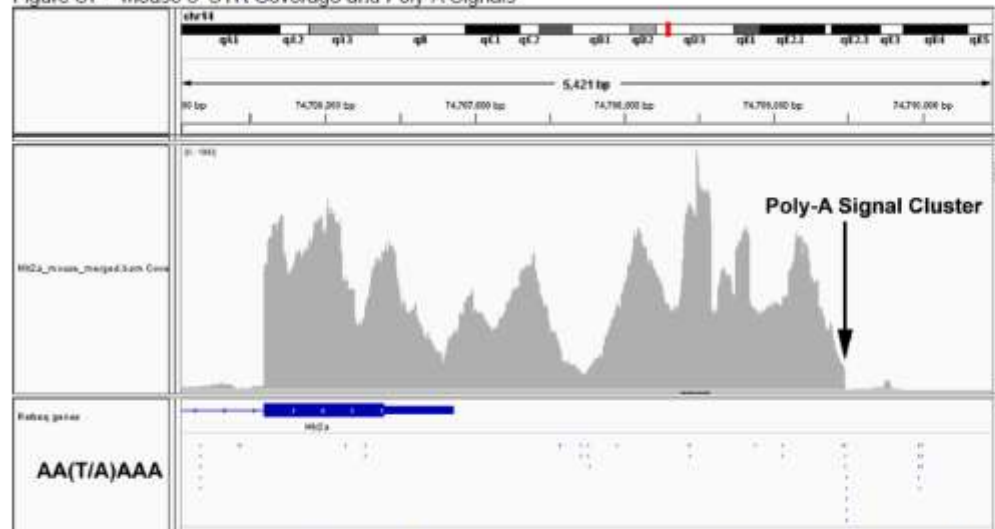


Figure S7 – Mouse 3' UTR Coverage and Poly-A Signals



**Figure S6.** Composite of mapped reads across all mouse tissues for the 3' UTR. The depth of mapped reads is indicated by the gray histogram in the upper panel, while *Htr2a* gene structure is depicted in the lower panel (5'-to-3' direction from left-to-right). The histogram depicts reads extending approximately 2.6 kB beyond the annotated terminus of *Htr2a*, continuing to a cluster of canonical and non-canonical poly-A signals (blue dots in lower panel). *Note:* read depth is presented in linear scale.